SEQUENCE LISTING

<110> JAPAN TOBACCO INC. and NORINSUISAN-SENTANGIJYUTU SANGYOUSHINKOU CENTOR

<120> A novel protein, a gene coding therefor and a method of using the same

<130> PC/N(x)-61-17

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<212> DNA

<213> Lyophyllum shimeji

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tct atg caa atc aac gga cag att cct aag aac gca att cac gaa aca    97
Ser Met Gln Ile Asn Gly Gln Ile Pro Lys Asn Ala Ile His Glu Thr
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tac gga aac gac gga gtt gat gta ttc att gca gga tct gga ccc att   145
Tyr Gly Asn Asp Gly Val Asp Val Phe Ile Ala Gly Ser Gly Pro Ile
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gga gcg acg tat gca aag ctc tgt gtt gaa gct ggt cta cgt gtt gtg   193
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atg gtc gag atc gga gct gct gat agc ttc tac gct gtt aat gcc gaa 241

Met Val Glu Ile Gly Ala Ala Asp Ser Phe Tyr Ala Val Asn Ala Glu

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gaa gga act gca gtt ccc tac gtt cct ggc tac cac aag aag aat gaa 289

Glu Gly Thr Ala Val Pro Tyr Val Pro Gly Tyr His Lys Lys Asn Glu

80 85 90

atc gag ttc cag aaa gat att gac cgc ttc gtc aat gta atc aag gga 337

Ile Glu Phe Gln Lys Asp Ile Asp Arg Phe Val Asn Val Ile Lys Gly

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gcc tta caa caa gtc tct gtt cct gtc aga aac cag aac gtg cct aca 385

Ala Leu Gln Gln Val Ser Val Pro Val Arg Asn Gln Asn Val Pro Thr

115 120 125

ctt gat ccc gga gcc tgg agc gcg ccc cct gga agt tca gcc ata tcg 433

Leu Asp Pro Gly Ala Trp Ser Ala Pro Pro Gly Ser Ser Ala Ile Ser

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aac ggt aaa aat cct cac cag cgg gaa ttc gag aac ttg tct gcg gag 481

Asn Gly Lys Asn Pro His Gln Arg Glu Phe Glu Asn Leu Ser Ala Glu

145 150 155

gcc gta acg cgt gga gtc ggc ggc atg agt acc cac tgg acg tgc tcc 529

Ala Val Thr Arg Gly Val Gly Gly Met Ser Thr His Trp Thr Cys Ser

160 165 170

acg cca cgg att cat cca ccc atg gaa agt ctc ccg ggc atc ggc cgt 577

Thr Pro Arg Ile His Pro Pro Met Glu Ser Leu Pro Gly Ile Gly Arg

175 180 185 190

ccg aag ctc agt aac gac ccg gca gag gac gac aaa gag tgg aac gag 625

Pro Lys Leu Ser Asn Asp Pro Ala Glu Asp Asp Lys Glu Trp Asn Glu

195 200 205

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Leu Tyr Ser Glu Ala Glu Arg Leu Ile Gly Thr Ser Thr Lys Glu Phe
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gac gag tca att cgg cac acc ctt gtt ctg cgc tct ttg caa gac gcg 721
Asp Glu Ser Ile Arg His Thr Leu Val Leu Arg Ser Leu Gln Asp Ala
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tac aag gat cgt caa cgt atc ttt cgc cct ctc ccg ttg gca tgc cac 769
Tyr Lys Asp Arg Gln Arg Ile Phe Arg Pro Leu Pro Leu Ala Cys His
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cgg ttg aag aac gcg ccg gaa tac gtc gaa tgg cac tca gca gaa aat 817
Arg Leu Lys Asn Ala Pro Glu Tyr Val Glu Trp His Ser Ala Glu Asn
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ctt ttc cac tct atc tac aac gat gac aag cag aag aag ctc ttt acc 865
Leu Phe His Ser Ile Tyr Asn Asp Asp Lys Gln Lys Lys Leu Phe Thr
275 280 285

ctg ctg acg aac cat cgc tgc aca cga ctg gcg ctt acg ggc ggg tat 913
Leu Leu Thr Asn His Arg Cys Thr Arg Leu Ala Leu Thr Gly Gly Tyr
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gag aag aag att ggc gct gcc gag gtc agg aat cta ctg gcc acc agg 961
Glu Lys Lys Ile Gly Ala Ala Glu Val Arg Asn Leu Leu Ala Thr Arg
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aat cct agt tcg cag ctg gac agc tat atc atg gcg aag gta tat gta 1009
Asn Pro Ser Ser Gln Leu Asp Ser Tyr Ile Met Ala Lys Val Tyr Val
320 325 330

ctg gcg tcg gga gcg atc ggc aac cca cag att ctc tat aac tcg ggc 1057
Leu Ala Ser Gly Ala Ile Gly Asn Pro Gln Ile Leu Tyr Asn Ser Gly
335 340 345 350

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Leu Arg Gln Glu Phe Val Asp Ser Val Arg Asp Asp Pro Tyr Gly Leu
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cca tgg tgg aaa gaa gcc gtt gct caa cat att gcc aag aac ccg aca  1249
Pro Trp Trp Lys Glu Ala Val Ala Gln His Ile Ala Lys Asn Pro Thr
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gat gca ctg ccc att ccg ttc cgc gat ccg gaa ccc cag gta aca acc  1297
Asp Ala Leu Pro Ile Pro Phe Arg Asp Pro Glu Pro Gln Val Thr Thr
415                 420                 425                 430
cca ttt aca gaa gaa cac ccc tgg cac acg cag att cac cgc gat gct  1345
Pro Phe Thr Glu Glu His Pro Trp His Thr Gln Ile His Arg Asp Ala
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Phe Ser Tyr Gly Ala Val Gly Pro Glu Val Asp Ser Arg Val Ile Val
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Asp Leu Arg Trp Phe Gly Ala Thr Asp Pro Glu Ala Asn Asn Leu Leu
        465                 470                 475
gtt ttc cag aac gat gtt caa gac ggg tac agt atg ccg cag ccg acg  1489
Val Phe Gln Asn Asp Val Gln Asp Gly Tyr Ser Met Pro Gln Pro Thr
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ttc aga tat cga ccc agc act gcg tca aac gtg aga gca agg aaa atg  1537
Phe Arg Tyr Arg Pro Ser Thr Ala Ser Asn Val Arg Ala Arg Lys Met
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atg gcc gat atg tgc gaa gtg gcg agc aac ttg gga ggt tat ttg ccc  1585
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Met Ala Asp Met Cys Glu Val Ala Ser Asn Leu Gly Gly Tyr Leu Pro
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acg tcc ccc ccg cag ttt atg gat cca ggc ctt gca ctt cat ctt gcg 1633
Thr Ser Pro Pro Gln Phe Met Asp Pro Gly Leu Ala Leu His Leu Ala
530 535 540

ggg act act cgc att ggc ttc gac aag gca act aca gtg gct gat aac 1681
Gly Thr Thr Arg Ile Gly Phe Asp Lys Ala Thr Thr Val Ala Asp Asn
545 550 555

aac tcg ctg gtc tgg gac ttt gcc aat ctt tat gtt gca ggc aat ggc 1729
Asn Ser Leu Val Trp Asp Phe Ala Asn Leu Tyr Val Ala Gly Asn Gly
560 565 570

acc atc agg acg ggc ttc ggc gag aac ccg aca ctt acg tcg atg tgc 1777
Thr Ile Arg Thr Gly Phe Gly Glu Asn Pro Thr Leu Thr Ser Met Cys
575 580 585 590

cac gct atc aag agc gcg agg agc atc atc aat aca ctc aag ggt ggg 1825
His Ala Ile Lys Ser Ala Arg Ser Ile Ile Asn Thr Leu Lys Gly Gly
595 600 605

act gac gga aaa aat aca ggc gag cat cgc aac ctt tga ggaaggagca ac 1876
Thr Asp Gly Lys Asn Thr Gly Glu His Arg Asn Leu
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Tyr Gly Asn Asp Gly Val Asp Val Phe Ile Ala Gly Ser Gly Pro
            35   40   45

Ile Gly Ala Thr Tyr Ala Lys Leu Cys Val Glu Ala Gly Leu Arg
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Val Val Met Val Glu Ile Gly Ala Ala Asp Ser Phe Tyr Ala Val
            65   70   75

Asn Ala Glu Glu Gly Thr Ala Val Pro Tyr Val Pro Gly Tyr His
            80   85   90

Lys Lys Asn Glu Ile Glu Phe Gln Lys Asp Ile Asp Arg Phe Val
            95   100   105

Asn Val Ile Lys Gly Ala Leu Gln Gln Val Ser Val Pro Val Arg
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Asn Gln Asn Val Pro Thr Leu Asp Pro Gly Ala Trp Ser Ala Pro
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Pro Gly Ser Ser Ala Ile Ser Asn Gly Lys Asn Pro His Gln Arg
            140   145   150

Glu Phe Glu Asn Leu Ser Ala Glu Ala Val Thr Arg Gly Val Gly
            155   160   165

Gly Met Ser Thr His Trp Thr Cys Ser Thr Pro Arg Ile His Pro
            170   175   180

Pro Met Glu Ser Leu Pro Gly Ile Gly Arg Pro Lys Leu Ser Asn
            185   190   195

Asp Pro Ala Glu Asp Asp Lys Glu Trp Asn Glu Leu Tyr Ser Glu

200 205 210

Ala Glu Arg Leu Ile Gly Thr Ser Thr Lys Glu Phe Asp Glu Ser

215 220 225

Ile Arg His Thr Leu Val Leu Arg Ser Leu Gln Asp Ala Tyr Lys

230 235 240

Asp Arg Gln Arg Ile Phe Arg Pro Leu Pro Leu Ala Cys His Arg

245 250 255

Leu Lys Asn Ala Pro Glu Tyr Val Glu Trp His Ser Ala Glu Asn

260 265 270

Leu Phe His Ser Ile Tyr Asn Asp Asp Lys Gln Lys Lys Leu Phe

275 280 285

Thr Leu Leu Thr Asn His Arg Cys Thr Arg Leu Ala Leu Thr Gly

290 295 300

Gly Tyr Glu Lys Lys Ile Gly Ala Ala Glu Val Arg Asn Leu Leu

305 310 315

Ala Thr Arg Asn Pro Ser Ser Gln Leu Asp Ser Tyr Ile Met Ala

320 325 330

Lys Val Tyr Val Leu Ala Ser Gly Ala Ile Gly Asn Pro Gln Ile

335 340 345

Leu Tyr Asn Ser Gly Phe Ser Gly Leu Gln Val Thr Pro Arg Asn

350 355 360

Asp Ser Leu Ile Pro Asn Leu Gly Arg Tyr Ile Thr Glu Gln Pro

365 370 375

Met Ala Phe Cys Gln Ile Val Leu Arg Gln Glu Phe Val Asp Ser

380 385 390

Val Arg Asp Asp Pro Tyr Gly Leu Pro Trp Trp Lys Glu Ala Val

395 400 405

Ala Gln His Ile Ala Lys Asn Pro Thr Asp Ala Leu Pro Ile Pro

410 415 420

Phe Arg Asp Pro Glu Pro Gln Val Thr Thr Pro Phe Thr Glu Glu
425 430 435
His Pro Trp His Thr Gln Ile His Arg Asp Ala Phe Ser Tyr Gly
440 445 450
Ala Val Gly Pro Glu Val Asp Ser Arg Val Ile Val Asp Leu Arg
455 460 465
Trp Phe Gly Ala Thr Asp Pro Glu Ala Asn Asn Leu Leu Val Phe
470 475 480
Gln Asn Asp Val Gln Asp Gly Tyr Ser Met Pro Gln Pro Thr Phe
485 490 495
Arg Tyr Arg Pro Ser Thr Ala Ser Asn Val Arg Ala Arg Lys Met
500 505 510
Met Ala Asp Met Cys Glu Val Ala Ser Asn Leu Gly Gly Tyr Leu
515 520 525
Pro Thr Ser Pro Pro Gln Phe Met Asp Pro Gly Leu Ala Leu His
530 535 540
Leu Ala Gly Thr Thr Arg Ile Gly Phe Asp Lys Ala Thr Thr Val
545 550 555
Ala Asp Asn Asn Ser Leu Val Trp Asp Phe Ala Asn Leu Tyr Val
560 565 570
Ala Gly Asn Gly Thr Ile Arg Thr Gly Phe Gly Glu Asn Pro Thr
575 580 585
Leu Thr Ser Met Cys His Ala Ile Lys Ser Ala Arg Ser Ile Ile
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Asn Thr Leu Lys Gly Gly Thr Asp Gly Lys Asn Thr Gly Glu His
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Arg Asn Leu
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Gln Asp Ala Tyr Lys Asp Arg Gln Arg
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Asp Arg Gln Arg

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